Please replace the paragraph beginning at page 8, line 14, with the following rewritten paragraph:

-- Figure 3 compares the sequence of the HER2/neu promoter (main chain - positions 462-491 of SEQ ID NO:6; complementary chain - SEQ ID NO:7) and polyamide structures and binding sites; the binding site for the TATA binding protein (TBP) is indicated along with the structures of the polyamides HER2-A, HER2-1, 70, and the mismatch polyamide 86. --

Please replace the paragraph beginning at page 9, line 1, with the following rewritten paragraph:

-- Figure 7 shows binding models for polyamides **1a-1c**. The double-stranded DNA sequence encompassing the HER 2/neu TATA element (main chain - positions 474-487 of SEQ ID NO:6; complementary chain - SEQ ID NO:8) and flaking sequence is shown, with the TATA element boxed. Polyamides are represented schematically between the two DNA strands at their respective binding sites. The closed and open circles represent Im and Py rings, respectively, the diamonds represent β-alanine (β) and the curved lines represent γ-aminobutyric acid (γ). The charged chiral turn ((R)-2,4-diaminobutyric acid) is represented with a plus sign as is the terminal dimethylaminopropylamide. Equilibrium association constants for each polyamide were determined by quantitative DNase I footprinting and are indicated. --

Please replace the paragraph beginning at page 22, line 16, with the following rewritten paragraph:

-- Electrophoretic Mobility Shift Assays (EMSA) were performed to determine whether the addition of various concentrations of polyamides specific for the sequences flanking the TATA box of the HRT2/neu promoter could interfere with the DNA binding activity of the TATA dinding protein (TBP). Oligonucleotides corresponding to the HER2/neu TATA box and

the adjacent sequences were synthesized. The first oligonucleotide, HERTATA1, has the sequence 5'-GCTGCTTGAGGAAGTATAAGAATGAAGTTGTGAAG-3' (SEQ ID NO:2) (the TATA box is in bold). The complementary oligonucleotide, HERTATA2, has the sequence 5'-CTTCACAACTTCATTCTTATACTTCCTCAAGCAGC-3' (SEQ ID NO:3). These complementary 35 base oligonucleotides were 5' end-labeled with γ-^{32}P-ATP and T4 polynucleotide kinase and then annealed to give a double-stranded 35 base pair oligonucleotide. This oligonucleotide was then used in electrophoretic mobility shift assays employing 5% nondenaturing polyacrylamide gels (29:1 acrylamide to bisacrylamide) containing 4mM $MgCl_2$ and 0.02% (v/v) NP-40 nonionic detergent along with 44 mM Tris-borate, pH 8.3, 1mM EDTA. The labeled oligo, at a concentration of 0.1 nM, was reacted with 1 nM final concentration of TBP (Promega) in a reaction volume of 20 µl, containing 10% glycerol (v/v), 20 mM HEPES-OH, pH 7.9, 25 mM KCL, 0.025% NP-40 (v/v), 100 µg/ml bovine serum albumin, 0.5 mM dithiothreitol, 0.8 mM spermidine, 0.1 mM EDTA, 2 mM $MgCl_2$. --

Please replace the paragraph beginning at page 25, line 14, with the following rewritten paragraph:

-- The effects of polyamide addition were subsequently analyzed using reverse transkriptase (RT)-polymerase chain reaction (PCR) as an assay for the relative level of HER2/neu mRNA. These HER2/neu mRNA levels should correlate with the amount of transcription from the HER2/neu promoter, allowing the determination of whether polyamide HER2-1 has any effect on transcription *in vivo*. Using PCR primers specific for the HER2/neu oncogene, the PCR product will correspond to HER2/neu cDNA, reflecting the relative levels of HER2/neu mRNA. The PCR primers were: (HER2A) 5'-GCTGGCCCGATGTATTTGATGGT-3' (SEQ ID NO:4) and (HER2B) 5'-GTTCTCTGCCGTAGGTGTCCCTTT-3' (SEQ ID NO:5), and 50 ng of each were used in PCR reactions as described below. --